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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/808,212A

DATE: 03/27/2002
TIME: 14:54:05

Input Set : A:\414us.app.txt
Output Set: N:\CRF3\03272002\I808212A.raw

4 <110> APPLICANT: Gore, Michael Graham
5 Beckingham, Jennifer Ann
6 Roberts, Sian Eleri
9 <120> TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN
12 <130> FILE REFERENCE: 100084.414US
14 <140> CURRENT APPLICATION NUMBER: 09/808,212A
15 <141> CURRENT FILING DATE: 2001-03-13
17 <160> NUMBER OF SEQ ID NOS: 32
19 <170> SOFTWARE: FastSEQ for Windows Version 4.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 249
23 <212> TYPE: DNA
24 <213> ORGANISM: Peptostreptococcus sp.
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (1)...(246)
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31 atg aac att aaa ttt gct gga aaa gaa aca cca gaa aca cca gaa gaa 48
32 Met Asn Ile Lys Phe Ala Gly Lys Glu Thr Pro Glu Thr Pro Glu Glu
33 1 5 10 15
35 cca aaa gaa gaa gtt aca atc aaa gtt aac tta atc ttt gca gat gga 96
36 Pro Lys Glu Glu Val Thr Ile Lys Val Asn Leu Ile Phe Ala Asp Gly
37 20 25 30
39 aag ata caa aca gca gaa ttc aaa gga aca ttt gaa gaa gca aca gca 144
40 Lys Ile Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala
41 35 40 45
43 gaa gct tac aga tat gca gac tta tta gca aaa gta aat ggc gaa tat 192
44 Glu Ala Tyr Arg Tyr Ala Asp Leu Leu Ala Lys Val Asn Gly Glu Tyr
45 50 55 60
47 aca gca gac tta gaa gat ggt gga aac cat atg aac att aaa ttt gct 240
48 Thr Ala Asp Leu Glu Asp Gly Gly Asn His Met Asn Ile Lys Phe Ala
49 65 70 75 80
51 gga aaa taa 249
52 Gly Lys
56 <210> SEQ ID NO: 2
57 <211> LENGTH: 82
58 <212> TYPE: PRT
59 <213> ORGANISM: Peptostreptococcus sp.
61 <400> SEQUENCE: 2
62 Met Asn Ile Lys Phe Ala Gly Lys Glu Thr Pro Glu Thr Pro Glu Glu
63 1 5 10 15
64 Pro Lys Glu Glu Val Thr Ile Lys Val Asn Leu Ile Phe Ala Asp Gly
65 20 25 30

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66 Lys Ile Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala
67 35 40 45
68 Glu Ala Tyr Arg Tyr Ala Asp Leu Leu Ala Lys Val Asn Gly Glu Tyr
69 50 55 60
70 Thr Ala Asp Leu Glu Asp Gly Gly Asn His Met Asn Ile Lys Phe Ala
71 65 70 75 80
72 Gly Lys
76 <210> SEQ ID NO: 3
77 <211> LENGTH: 228
78 <212> TYPE: DNA
79 <213> ORGANISM: *Peptostreptococcus* sp.
81 <220> FEATURE:
82 <221> NAME/KEY: CDS
83 <222> LOCATION: (1)...(228)
85 <400> SEQUENCE: 3
86 aaa gaa gaa aca cca gaa aca cca gaa act gat tca gaa gaa gaa gta 48
87 Lys Glu Glu Thr Pro Glu Thr Pro Glu Thr Asp Ser Glu Glu Glu Val
88 1 5 10 15
90 aca atc aaa gct aac cta atc ttt gca aat gga agc aca caa act gca 96
91 Thr Ile Lys Ala Asn Leu Ile Phe Ala Asn Gly Ser Thr Gln Thr Ala
92 20 25 30
94 gaa ttc aaa gga aca ttt gaa aaa gca aca tca gaa gct tat gcg tat 144
95 Glu Phe Lys Gly Thr Phe Glu Lys Ala Thr Ser Glu Ala Tyr Ala Tyr
96 35 40 45
98 gca gat act ttg aag aaa gac aat gga gaa tat act gta gat gtt gca 192
99 Ala Asp Thr Leu Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val Ala
100 50 55 60
102 gat aaa ggt tat act tta aat att aaa ttt gct gga 228
103 Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly
104 65 70 75
107 <210> SEQ ID NO: 4
108 <211> LENGTH: 76
109 <212> TYPE: PRT
110 <213> ORGANISM: *Peptostreptococcus* sp.
112 <400> SEQUENCE: 4
113 Lys Glu Glu Thr Pro Glu Thr Pro Glu Thr Asp Ser Glu Glu Glu Val
114 1 5 10 15
115 Thr Ile Lys Ala Asn Leu Ile Phe Ala Asn Gly Ser Thr Gln Thr Ala
116 20 25 30
117 Glu Phe Lys Gly Thr Phe Glu Lys Ala Thr Ser Glu Ala Tyr Ala Tyr
118 35 40 45
119 Ala Asp Thr Leu Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val Ala
120 50 55 60
121 Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly
122 65 70 75
125 <210> SEQ ID NO: 5
126 <211> LENGTH: 216
127 <212> TYPE: DNA
128 <213> ORGANISM: *Peptostreptococcus* sp.

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Input Set : A:\414us.app.txt
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130 <220> FEATURE:
131 <221> NAME/KEY: CDS
132 <222> LOCATION: (1)...(216)
134 <400> SEQUENCE: 5
135 aaa gaa aaa aca cca gaa gaa cca aaa gaa gaa gtt act att aaa gca 48
136 Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala
137 1 5 10 15
139 aac tta atc tat gca gat gga aaa aca caa aca gca gaa ttc aaa gga 96
140 Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
141 20 25 30
143 aca ttt gaa gaa gca aca gca gaa gca tac aga tat gca gat gca tta 144
144 Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Ala Leu
145 35 40 45
147 aag aag gac aat gga gaa tat aca gta gac gtt gca gat aaa ggt tat 192
148 Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr
149 50 55 60
151 act tta aat att aaa ttt gct gga 216
152 Thr Leu Asn Ile Lys Phe Ala Gly
153 65 70
156 <210> SEQ ID NO: 6
157 <211> LENGTH: 72
158 <212> TYPE: PRT
159 <213> ORGANISM: Peptostreptococcus sp.
161 <400> SEQUENCE: 6
162 Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala
163 1 5 10 15
164 Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
165 20 25 30
166 Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Ala Leu
167 35 40 45
168 Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr
169 50 55 60
170 Thr Leu Asn Ile Lys Phe Ala Gly
171 65 70
174 <210> SEQ ID NO: 7
175 <211> LENGTH: 216
176 <212> TYPE: DNA
177 <213> ORGANISM: Peptostreptococcus sp.
179 <220> FEATURE:
180 <221> NAME/KEY: CDS
181 <222> LOCATION: (1)...(216)
183 <400> SEQUENCE: 7
184 aaa gaa aaa aca cca gaa gaa cca aaa gaa gaa gtt act att aaa gca 48
185 Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala
186 1 5 10 15
188 aac tta atc tat gca gat gga aaa aca caa aca gca gaa ttc aaa gga 96
189 Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
190 20 25 30
192 aca ttt gaa gaa gca aca gca gaa gca tac aga tat gct gac tta tta 144

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Input Set : A:\414us.app.txt

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193 Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu
 194 35 40 45
 196 gca aaa gaa aat ggt aaa tat aca gta gac gtt gca gat aaa ggt tat 192
 197 Ala Lys Glu Asn Gly Lys Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr
 198 50 55 60
 200 act tta aat att aaa ttt gct gga 216
 201 Thr Leu Asn Ile Lys Phe Ala Gly
 202 65 70
 205 <210> SEQ ID NO: 8
 206 <211> LENGTH: 72
 207 <212> TYPE: PRT
 208 <213> ORGANISM: *Peptostreptococcus* sp.
 210 <400> SEQUENCE: 8
 211 Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala
 212 1 5 10 15
 213 Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
 214 20 25 30
 215 Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu
 216 35 40 45
 217 Ala Lys Glu Asn Gly Lys Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr
 218 50 55 60
 219 Thr Leu Asn Ile Lys Phe Ala Gly
 220 65 70
 223 <210> SEQ ID NO: 9
 224 <211> LENGTH: 216
 225 <212> TYPE: DNA
 226 <213> ORGANISM: *Peptostreptococcus* sp.
 228 <220> FEATURE:
 229 <221> NAME/KEY: CDS
 230 <222> LOCATION: (1)...(216)
 232 <400> SEQUENCE: 9
 233 aaa gaa aaa aca cca gaa gaa cca aaa gaa gaa gtt act att aaa gca 48
 234 Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala
 235 1 5 10 15
 237 aac tta atc tat gca gat gga aaa act caa aca gca gag ttc aaa gga 96
 238 Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
 239 20 25 30
 241 aca ttt gca gaa gca aca gca gaa gca tac aga tac gct gac tta tta 144
 242 Thr Phe Ala Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu
 243 35 40 45
 245 gca aaa gaa aat ggt aaa tat aca gca gac tta gaa gat ggt gga tac 192
 246 Ala Lys Glu Asn Gly Lys Tyr Thr Ala Asp Leu Glu Asp Gly Gly Tyr
 247 50 55 60
 249 act att aat att aga ttt gca ggt 216
 250 Thr Ile Asn Ile Arg Phe Ala Gly
 251 65 70
 254 <210> SEQ ID NO: 10
 255 <211> LENGTH: 72
 256 <212> TYPE: PRT

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Input Set : A:\414us.app.txt
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257 <213> ORGANISM: *Peptostreptococcus* sp.
 259 <400> SEQUENCE: 10
 260 Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala
 261 1 5 10 15
 262 Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
 263 20 25 30
 264 Thr Phe Ala Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu
 265 35 40 45
 266 Ala Lys Glu Asn Gly Lys Tyr Thr Ala Asp Leu Glu Asp Gly Gly Tyr
 267 50 55 60
 268 Thr Ile Asn Ile Arg Phe Ala Gly
 269 65 70
 272 <210> SEQ ID NO: 11
 273 <211> LENGTH: 213
 274 <212> TYPE: DNA
 275 <213> ORGANISM: *Peptostreptococcus* sp.
 277 <220> FEATURE:
 278 <221> NAME/KEY: CDS
 279 <222> LOCATION: (1)...(213)
 281 <400> SEQUENCE: 11
 282 aaa gaa aca cca gaa cca gaa gaa gaa gtt aca atc aaa gct aac tta 48
 283 Lys Glu Thr Pro Glu Pro Glu Glu Val Thr Ile Lys Ala Asn Leu
 284 1 5 10 15
 286 atc ttt gca gat gga agc aca caa aat gca gaa ttc aaa gga aca ttc 96
 287 Ile Phe Ala Asp Gly Ser Thr Gln Asn Ala Glu Phe Lys Gly Thr Phe
 288 20 25 30
 290 gca aaa gca gta tca gat gct tac gct gca gat gct tta aag aaa 144
 291 Ala Lys Ala Val Ser Asp Ala Tyr Ala Tyr Ala Asp Ala Leu Lys Lys
 292 35 40 45
 294 gac aac gga gaa tat act gta gac gtt gca gat aaa ggc tta act tta 192
 295 Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Leu Thr Leu
 296 50 55 60
 298 aat att aaa ttc gct ggt aaa 213
 299 Asn Ile Lys Phe Ala Gly Lys
 300 65 70
 303 <210> SEQ ID NO: 12
 304 <211> LENGTH: 71
 305 <212> TYPE: PRT
 306 <213> ORGANISM: *Peptostreptococcus* sp.
 308 <400> SEQUENCE: 12
 309 Lys Glu Thr Pro Glu Pro Glu Glu Val Thr Ile Lys Ala Asn Leu
 310 1 5 10 15
 311 Ile Phe Ala Asp Gly Ser Thr Gln Asn Ala Glu Phe Lys Gly Thr Phe
 312 20 25 30
 313 Ala Lys Ala Val Ser Asp Ala Tyr Ala Tyr Ala Asp Ala Leu Lys Lys
 314 35 40 45
 315 Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Leu Thr Leu
 316 50 55 60
 317 Asn Ile Lys Phe Ala Gly Lys

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/808,212A

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Input Set : A:\414us.app.txt

Output Set: N:\CRF3\03272002\I808212A.raw